Visualization Tools:

A new interactive heatmap program "Dynamic Heatmap Viewer" written in C++ was created to replace current implementation in clustering genes and sample tool. The new program allows users to explore gene expression by visualizing the heatmap of data interactively through simple-to-use graphical user interface. Some of features include zoom-in of heatmap, real-time change of gene ID and array label from mouse-over gene and array, displaying sample class along with heatmap, and so on. The previously existing "Heatmap of Data" tool is deprecated.

Added color-coding KEGG pathway graph functionality to Class Comparison and Gene Set Analysis tools. This new tool provides a powerful visualization tool to discover up- or down-regulated genes in KEGG pathways.

Analysis Tools:

Developed a new module in Class Comparison and Quantitative Trait Analysis tools to automatically create Ingenuity IPA output files to be imported into Ingenuity IPA.

Updated Broad MSigDB collections to the latest v4.0 version. Modified Broad MSigDB download module to allow users easily update the download link themselves.

Separated the MIR and TFT gene sets in Broad MSigDB C3 motif gene sets. Modified code to center and scale genes after hierarchical cluster analysis is performed. Centering and scaling is only conducted for the purpose of generating a heatmap.

Importing, Filtering, Normalization and Annotation:

Added the option to allow importing custom Gene Identifiers files for annotation with files in mAdb format.

Installation, Registration and Support Links:

Modified the license key file structure to improve security.